

SEQUENCE LISTING



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(1) GENERAL INFORMATION:

(i) APPLICANTS: Hein, Mich B.
Hiatt, Andrew C.
Fitchen, John H.

(ii) TITLE OF INVENTION: NOVEL EPITHELIAL TISSUE TARGETING AGENT

(iii) NUMBER OF SEQUENCES: 140

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SEED IP LAW GROUP PLLC
(B) STREET: 701 Fifth Avenue, Suite 6300
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: USA
(F) ZIP: 98104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/005,318
(B) FILING DATE: 09-JAN-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Christiansen, William T.
(B) REGISTRATION NUMBER: 44,614
(C) REFERENCE/DOCKET NUMBER: 310098.401C1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 622-4900
(B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys Ala
 1 5 10 15
 Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu Asp
 20 25 30
 Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg Glu
 35 40 45
 Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Pro Val Tyr His
 50 55 60
 Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp
 65 70 75 80
 Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser
 85 90 95
 Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Ala
 100 105 110
 Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val Glu Thr Ala
 115 120 125
 Leu Thr Pro Asp Ala Cys Tyr Pro Asp
 130 135

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gln Asp Glu Asn Glu Arg Ile Val Val Asp Asn Lys Cys Lys Cys Ala
 1 5 10 15
 Arg Ile Thr Ser Arg Ile Ile Pro Ser Ala Glu Asp Pro Ser Gln Asp
 20 25 30
 Ile Val Glu Arg Asn Val Arg Ile Ile Val Pro Leu Asn Ser Arg Glu
 35 40 45
 Asn Ile Ser Asp Pro Thr Ser Pro Met Arg Thr Lys Pro Val Tyr His
 50 55 60

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Leu Ser Asp Leu Cys Lys Lys Cys Asp Thr Thr Glu Val Glu Leu Glu
65                      70                      75                      80

Asp Gln Val Val Thr Ala Ser Gln Ser Asn Ile Cys Asp Ser Asp Ala
                        85                      90                      95

Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Asn Arg Val
                        100                     105                     110

Lys Leu Ser Tyr Arg Gly Gln Thr Lys Met Val Glu Thr Ala Leu Thr
                        115                     120                     125

Pro Asp Ser Cys Tyr Pro Asp
                        130                     135

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

Asp Asp Glu Ala Thr Ile Leu Ala Asp Asn Lys Cys Met Cys Thr Arg
1                      5                      10                      15

Val Thr Ser Arg Ile Ile Pro Ser Thr Glu Asp Pro Asn Glu Asp Ile
                        20                      25                      30

Val Glu Arg Asn Ile Arg Ile Val Val Pro Leu Asn Asn Arg Glu Asn
                        35                      40                      45

Ile Ser Asp Pro Thr Ser Pro Leu Arg Arg Asn Pro Val Tyr His Leu
50                      55                      60

Ser Asp Val Cys Lys Lys Cys Asp Pro Val Glu Val Glu Leu Glu Asp
65                      70                      75                      80

Gln Val Val Thr Ala Thr Gln Ser Asn Ile Cys Asn Glu Asp Asp Gly
                        85                      90                      95

Val Pro Glu Thr Cys Tyr Met Tyr Asp Arg Asn Lys Cys Tyr Thr Thr
100                     105                     110

Met Val Pro Leu Arg Tyr His Gly Glu Thr Lys Met Val Gln Ala Ala
115                     120                     125

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Leu Thr Pro Asp Ser Cys Tyr Pro Asp
130 135

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Asp Glu Ser Thr Val Leu Val Asp Asn Lys Cys Gln Cys Val Arg
1 5 10 15

Ile Thr Ser Arg Ile Ile Arg Asp Pro Asp Asn Pro Ser Glu Asp Ile
20 25 30

Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Thr Arg Glu Asn
35 40 45

Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Glu Pro Lys Tyr Asn Leu
50 55 60

Ala Asn Leu Cys Lys Lys Cys Asp Pro Thr Glu Ile Glu Leu Asp Asn
65 70 75 80

Gln Val Phe Thr Ala Ser Gln Ser Asn Ile Cys Pro Asp Asp Asp Tyr
85 90 95

Ser Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Thr Leu
100 105 110

Val Pro Ile Thr His Arg Gly Val Thr Arg Met Val Lys Ala Thr Leu
115 120 125

Thr Pro Asp Ser Cys Tyr Pro Asp
130 135

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Glu	Gln	Glu	Tyr	Ile	Leu	Ala	Asn	Asn	Lys	Cys	Lys	Cys	Val	Lys	Ile	1	5	10	15
Ser	Ser	Arg	Phe	Val	Pro	Ser	Thr	Glu	Arg	Pro	Gly	Glu	Glu	Ile	Leu	20	25	30	
Glu	Arg	Asn	Ile	Gln	Ile	Thr	Ile	Pro	Thr	Ser	Ser	Arg	Met	Xaa	Ile	35	40	45	
Ser	Asp	Pro	Tyr	Ser	Pro	Leu	Arg	Thr	Gln	Pro	Val	Tyr	Asn	Leu	Trp	50	55	60	
Asp	Ile	Cys	Gln	Lys	Cys	Asp	Pro	Val	Gln	Leu	Glu	Ile	Gly	Gly	Ile	65	70	75	80
Pro	Val	Leu	Ala	Ser	Gln	Pro	Xaa	Xaa	Ser	Xaa	Pro	Asp	Asp	Glu	Cys	85	90	95	
Tyr	Thr	Thr	Glu	Val	Asn	Phe	Lys	Lys	Lys	Val	Pro	Leu	Thr	Pro	Asp	100	105	110	
Ser	Cys	Tyr	Glu	Tyr	Ser	Glu	115												

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asn	Lys	Cys	Met	Cys	Thr	Arg	Val	Thr	Ala	Arg	Ile	Arg	Gly	Thr	Arg	1	5	10	15
Glu	Asp	Pro	Asn	Glu	Asp	Ile	Val	Glu	Arg	Tyr	Ile	Arg	Ile	Asn	Val	20	25	30	
Pro	Leu	Lys	Asn	Arg	Gly	Asn	Ile	Ser	Asp	Pro	Thr	Ser	Pro	Leu	Arg	35	40	45	
Asn	Gln	Pro	Val	Tyr	His	Leu	Ser	Pro	Ser	Cys	Lys	Lys	Cys	Asp	Pro				

50		55		60
Tyr Glu Asp Gly Val Val Thr Ala Thr Glu Thr Asn Ile Cys Tyr Pro				
65		70		75
				80
Asp Gln Gly Val Pro Gln Ser Cys Arg Asp Tyr Cys Pro Glu Leu Asp				
	85		90	95
Arg Asn Lys Cys Tyr Thr Val Leu Val Pro Pro Gly Tyr Thr Gly Glu				
	100		105	110
Thr Lys Met Val Gln Asn Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp				
	115		120	125

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAT CAG GAA GAT GAA CGT ATT GTT CTG GTT GAC AAC AAG TGC AAG TGT	48
Asp Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys	
1 5 10 15	
GCT CGT ATT ACT TCT AGA ATC ATC CGT AGC TCA GAG GAC CCA AAT GAA	96
Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu	
20 25 30	
GAT ATA GTC GAA CGT AAC ATC CGT ATC ATC GTC CCA CTG AAT AAC CGG	144
Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg	
35 40 45	
GAG AAT ATC TCA GAT CCT ACA AGT CCG TTG CGC ACA CGC TTC GTA TAC	192
Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val Tyr	
50 55 60	
CAC CTG TCA GAT CTG TGT AAG AAG TGT GAT CCA ACA GAG GTA GAG CTG	240
His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu	
65 70 75 80	
GAC AAT CAG ATA GTC ACT GCG ACT CAA AGC AAC ATT TGC GAT GAG GAC	288
Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp	

85								90					95			
AGC	GCT	ACA	GAA	ACC	TGC	AGC	ACC	TAC	GAT	AGG	AAC	AAA	TGC	TAC	ACG	336
Ser	Ala	Thr	Glu	Thr	Cys	Ser	Thr	Tyr	Asp	Arg	Asn	Lys	Cys	Tyr	Thr	
100								105					110			
GCC	GTG	GTT	CCG	CTC	GTG	TAT	GGT	GGA	GAG	ACA	AAA	ATG	GTG	GAA	ACT	384
Ala	Val	Val	Pro	Leu	Val	Tyr	Gly	Gly	Glu	Thr	Lys	Met	Val	Glu	Thr	
115								120					125			
GCC	CTT	ACG	CCC	GAT	GCA	TGC	TAT	CCG	GAC	TGAATTC						421
Ala	Leu	Thr	Pro	Asp	Ala	Cys	Tyr	Pro	Asp							
130								135								

(2) INFORMATION FOR SEO ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

[illegible]

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTAGAATCAT CCGTAGCTCA GAGGACCCAA ATGAAGATAT AGTCGAACGT AACATCCGTA 60
 TCATCGTCCC ACTGAATAAC CGGGAGAATA TCTCAGATCC TACAAGTCCG TTGCGCACAC 120
 GCTTCGTATA CCACCTGTCA 140

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GATCAGAAGT GCAAGTGTGC TCGTATTACT T 31

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAT CTG TGT AAG AAG GAT GAA GAT TCC GCT ACA GAA ACC TGC TG 44
 Asp Leu Cys Lys Lys Asp Glu Asp Ser Ala Thr Glu Thr Cys

1

5

10

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCACCTACGA TAGGAACAAA TGCTACACGG CCGTGGTTCC GCTCGTGTAT GGTGGAGAGA 60
 CAAAAATGGT GGAAACTGCC CTTACGCCCG ATGCATGCTA CCCTGACTG 109

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAT CAG AAG TGC AAG TGT GCT CGT ATT ACT TCT AGA ATC ATC CGT AGC 48
 Asp Gln Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser
 1 5 10 15

TCA GAG GAC CCA AAT GAA GAT ATA GTC GAA CGT AAC ATC CGT ATC ATC 96
 Ser Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile
 20 25 30

GTC CCA CTG AAT AAC CGG GAG AAT ATC TCA GAT CCT ACA AGT CCG TTG 144
 Val Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu
 35 40 45

CGC ACA CGC TTC GTA TAC CAC CTG TCA GAT CTG TGT AAG AAG TGT GAT 192

Arg	Thr	Arg	Phe	Val	Tyr	His	Leu	Ser	Asp	Leu	Cys	Lys	Lys	Cys	Asp	
50						55					60					
CCA	ACA	GAG	GTA	GAG	CTG	GAC	AAT	CAG	ATA	GTC	ACT	GCG	ACT	CAA	AGC	240
Pro	Thr	Glu	Val	Glu	Leu	Asp	Asn	Gln	Ile	Val	Thr	Ala	Thr	Gln	Ser	
65					70					75					80	
AAC	ATT	TGC	GAT	GAG	GAC	AGC	GCT	ACA	GAA	ACC	TGC	TAC	TGA	ATTC		286
Asn	Ile	Cys	Asp	Glu	Asp	Ser	Ala	Thr	Glu	Thr	Cys	Tyr				
				85					90							

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAT	CTG	TGT	AAG	AAG	TGT	GAT	CCA	ACA	GAG	GTA	GAG	CTG	GAC	AAT	CAG	48
Asp	Leu	Cys	Lys	Lys	Cys	Asp	Pro	Thr	Glu	Val	Glu	Leu	Asp	Asn	Gln	
1				5					10					15		
ATA	GTC	ACT	GCG	ACT	CAA	AGC	AAC	ATT	TGC	GAT	GAG	GAC	AGC	GCT	ACA	96
Ile	Val	Thr	Ala	Thr	Gln	Ser	Asn	Ile	Cys	Asp	Glu	Asp	Ser	Ala	Thr	
			20				25						30			
GAA	ACC	TGC														105
Glu	Thr	Cys														
			35													

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GATCAGGAAG ATGAACGTAT TGTCTGGTT GACAACAAGT GCAAGTGTGC TCGTATTACT 60
 T 61

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCGATGACGA CGATAAGGCC CAAACGGAGA CCTGTACTGT TGCGCCTCGT GAACGGCAAA 60
 ACTGCGGATT CCCGGAAGTA ACACCCTCTC AGTGCGCTAA TAAAGGCTGC TGTTTTGATG 120
 ACACGGTACG GGGCGTTCCG TGGTGCTTCT ACCCCAATAC AATTGACGTT CCGCCTGAAG 180
 AAGAGTGCGA GCCGTAAG 198

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Asp Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys
 1 5 10 15
 Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu
 20 25 30
 Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg
 35 40 45
 Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val Tyr
 50 55 60
 His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu

65		70		75		80									
Asp	Asn	Gln	Ile	Val	Thr	Ala	Thr	Gln	Ser	Asn	Ile	Cys	Asp	Glu	Asp
				85					90					95	
Ser	Ala	Thr	Glu	Thr	Cys	Ser	Thr	Tyr	Asp	Arg	Asn	Lys	Cys	Tyr	Thr
			100					105					110		
Ala	Val	Val	Pro	Leu	Val	Tyr	Gly	Gly	Glu	Thr	Lys	Met	Val	Glu	Thr
		115					120					125			
Ala	Leu	Thr	Pro	Asp	Ala	Cys	Tyr	Pro	Asp						
	130					135									

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asp	Gln	Lys	Cys	Lys	Cys	Ala	Arg	Ile	Thr	Ser	Arg	Ile	Ile	Arg	Ser
1				5					10					15	
Ser	Glu	Asp	Pro	Asn	Glu	Asp	Ile	Val	Glu	Arg	Asn	Ile	Arg	Ile	Ile
			20					25					30		
Val	Pro	Leu	Asn	Asn	Arg	Glu	Asn	Ile	Ser	Asp	Pro	Thr	Ser	Pro	Leu
		35					40					45			
Arg	Thr	Arg	Phe	Val	Tyr	His	Leu	Ser	Asp	Leu	Cys	Lys	Lys	Asp	Glu
	50					55					60				
Asp	Ser	Ala	Thr	Glu	Thr	Cys									
	65				70										

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu Asp Ile Val Glu
1 5 10 15

Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg Glu Asn Ile Ser
20 25 30

Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val Tyr His Leu Ser Asp
35 40 45

Leu

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Asp Gln Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEO ID NO:21:

Asp Leu Cys Lys Lys Asp Glu Asp Ser Ala Thr Glu Thr Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ser Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val
 1 5 10 15

Tyr Gly Gly Glu Thr Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala
 20 25 30

Cys Tyr Pro Asp
 35

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Asp Gln Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser
 1 5 10 15

Ser Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile
 20 25 30

Val Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu
 35 40 45

Arg Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp
 50 55 60

Pro Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser
 65 70 75 80

Asn Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr
 85 90

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp Asn Gln
 1 5 10 15
 Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser Ala Thr
 20 25 30
 Glu Thr Cys
 35

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asp Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys
 1 5 10 15
 Ala Arg Ile Thr Ser Arg
 20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys Ser Asp Asp Asp Asp Lys Ala Gln Thr Glu Thr Cys Thr Val Ala
 1 5 10 15
 Pro Arg Glu Arg Gln Asn Cys Gly Phe Pro Gly Val Thr Pro Ser Gln
 20 25 30

Cys Ala Asn Lys Gly Cys Cys Phe Asp Asp Thr Val Arg Gly Val Pro
 35 40 45
 Trp Cys Phe Tyr Pro Asn Thr Ile Asp Val Pro Pro Glu Glu Glu Cys
 50 55 60
 Glu Phe
 65

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTAGTCCTTC TACTTGCATA ACAAGACCAA CTGTTGTTCA CGTTCACACG AGCATAATGA	60
AGATCTTAGT AGGCATCGAG TCTCCTGGGT TTACTTCTAT ATCAGCTTGC ATTGTAGGCA	120
TAGTAGCAGG GTGACTTATT GGCCCTCTTA TAGAGTCTAG GATGTTCAGG CAACGCGTGT	180
GCGAAGCATA TGGTGGACAG TCTAGACACA TTCTTCACAC TAGGTTGTCT CCATCTCGAC	240
CTGTTAGTCT ATCAGTGACG CTGAGTTTCG TTGTAAACGC TACTCCTGTC GCGATGTCTT	300
TGGACGTCGT GGATGCTATC CTTGTTTACG ATGTGCCGGC ACCAAGGCGA GCACATACCA	360
CCTCTCTGTT TTTACCACCT TTGACGGGAA TGCGGGCTAC GTACGATAGG CCTGACTTAA	420
G	421

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTAGTCTTCA CGTTCACACG AGCATAATGA AGATCTTAGT AGGCATCGAG TCTCCTGGGT 60
 TTACTTCTAT ATCAGCTTGC ATTGTAGGCA TAGTAGCAGG GTGACTTATT GGCCCTCTTA 120
 TAGAGTCTAG GATGTTTCAGG CAACGCGTGT GCGAAGCATA TGGTGGACAG TCTAGACACA 180
 TTCTTCCTAC TCCTGTCGCG ATGTCTTTGG ACGACTTAA 219

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTAGTAGGCA TCGAGTCTCC TGGGTTTACT TCTATATCAG CTTGCATTGT AGGCATAGTA 60
 GCAGGGTGAC TTATTGGCCC TCTTATAGAG TCTAGGATGT TCAGGCAACG CGTGTGCGAA 120
 GCATATGGTG GACAGTCTAG 140

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TCTTCACGTT CACACGAGCA TAATGAAGAT C 31

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ACACATTCTT CCTACTTCTC AGGCGATGTC TTTGGACGAC TTAA

44

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ACGTCGTGGA TGCTATCCTT GTTTACGATG TGCCGGCACC AAGGCGAGCA CATACCACCT

60

CTCTGTTTTT ACCACCTTTG ACGGGAATGC GGGCTACGTA CGATGGGACT GACTTAA

117

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTAGTCTTCA CGTTCACACG AGCATAATGA AGATCTTAGT AGGCATCGAG TCTCCTGGGT

60

TTACTTCTAT ATCAGCTTGC ATTGTAGGCA TAGTAGCAGG GTGACTTATT GGCCCTCTTA

120

TAGAGTCTAG GATGTTTCAGG CAACGCGTGT GCGAAGCATA TGGTGGACAG TCTAGACACA

180

TTCTTCACAC TAGGTTGTCT CCATCTCGAC CTGTTAGTCT ATCAGTGACG CTGAGTTTCG

240

TTGTAAACGC TACTCCTGTC GCGATGTCTT TGGACGATGA CT

282

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTAGACACAT TCTTCACACT AGGTTGTCTC CATCTCGACC TGTTAGTCTA TCAGTGACGC 60

TGAGTTTCGT TGTAACGCT ACTCCTGTCG CGATGTCTTT GGACG 105

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CTAGTCCTTC TACTTGCATA ACAAGACCAA CTGTTGTTCA CGTTCACACG AGCATAATGA 60

AGATC 65

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ACTTCGCTAC TGCTGCTATT CCGGGTTTGC CTCTGGACAT GACAACGCGG AGCACTTGCC 60

GTTTTGACGC CTAAGGGCCT TCATTGTGGG AGAGTCACGC GATTATTTCC GACGACAAAA 120

CTACTGTGCC ATGCCCCGCA AGGCACCACG AAGATGGGGT TATGTTAACT GCAAGGCGGA 180

CTTCTTCTCA CGCTCGGCAT TCTTAA 206

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Asp	Gln	Glu	Asp	Glu	Arg	Ile	Val	Leu	Val	Asp	Asn	Lys
1				5					10			

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Glu	Asn	Leu	Tyr	Phe	Gln	Ser
1				5		

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Lys	Ala	His	Lys	Val	Asp	Met	Val	Gln	Tyr	Thr
1				5					10	

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Val Gln Tyr Thr
1

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Glu Lys Ala Val Ala Asp
1 5

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATG AAA TTC TTA GTC AAC GTT GCC CTT TTT ATG GTC GTA TAC ATT TCT	48
Met Lys Phe Leu Val Asn Val Ala Leu Phe Met Val Val Tyr Ile Ser	
1 5 10 15	
TAC ATC TAT GCG GAT CCG AGC TCG AGT GCT CTAGATCTGC AGCTGGTACC	98
Tyr Ile Tyr Ala Asp Pro Ser Ser Ser Ala	
20 25	

ATGGAATTCG AAGCTTGGAG TCGACTCTGC TGA

131

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met	Lys	Phe	Leu	Val	Asn	Val	Ala	Leu	Phe	Met	Val	Val	Tyr	Ile	Ser
1				5				10						15	
Tyr	Ile	Tyr	Ala	Asp	Pro	Ser	Ser	Ser	Ala						
			20					25							

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Lys Asp Glu Leu
1

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ala	Ile	Gln	Asp	Pro	Arg	Leu	Phe	Ala	Glu	Glu	Lys	Ala	Val	Ala	Asp
1				5				10					15		

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GATCAGGAAG ATGAACGTAT TGTCTGGTT GACAACAAGT GCAAGTGTGC TCGTATTACT 60
 T 61

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTAGAAGTAA TACGAGCACA CTTGCACTTG TTGTCAACCA GAACAATACG TTCATCTTCC 60
 T 61

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATCAGAAGT GCAAGTGTGC TCGTATTACT T 31

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTAGAAGTAA TACGAGCACA CTTGCACTTC T

31

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GATCAGGAAG ATGAACGTAT TGTTCCTGGTT GACAACAAGT GCAAGTCCGC TCGTATTACT

60

T

61

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTAGAAGTAA TACGAGCGGA CTTGCACTTG TTGTCAACCA GAACAATACG TTCATCTTCC

60

T

61

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GATCAGGAAG ATGAACGTAT TGTCTGGTT GACAACAAGT GCAAGGTTGC TCGTATTACT 60

T 61

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CTAGAAGTAA TACGAGCAAC CTTGCACTTG TTGTCAACCA GAACAATACG TTCATCTTCC 60

T 61

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTAGAATCAT CCGTAGCTCA GAGGACCCAA ATGAAGATAT AGTCGAA 47

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GATACGGATG TTACGTTTCA CTATATCTTC ATTTGGGTCC TCTGAGCTAC GGATGATT

58

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CGTAACATCC GTATCATCGT CCCACTGAAT AACCGGGAGA ATATCTCAG

49

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CGTAACATCC GTATCATCGT CCCACTGAAT AACCGGGAGC ACATCTCAG

49

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACGGACTTGT AGGATCTGAG ATATTCTCCC GGTATTTCAG TGGGACGAT

49

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACGGACTTGT AGGATCTGAG ATGTGCTCCC GGTATTTCAG TGGGACGAT

49

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATCCTACAAG TCCGTTGCGC ACACGCTTCG TATACCACCT GTCA

44

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GATCTGACAG GTGGTATACG AAGCGTGTGC GCA

33

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GATCTGTGTA AGAAGTGTGA TCCAACAGAG GTAGAGCTGG ACAATCAGAT AGTCACTGCA 60

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GATCTGTGTA AGAAGGATGA GGACAGCGCT ACAGAAACCT GCTG 44

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

AATTCAGCAG GTTTCTGTAG CGCTGTCCTC ATCCTTCTTA CACA 44

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GATCTGTGTA AGAAGGATGA GGACAGCGCT ACAGAAACCT GCTACGAGAA GGATGAGCTG 60
TG 62

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AATTCACAGC TCATCCTTCG CGTCGCAGGT TTCTGTAGCG CTGTCCTCAT CCTTCTTACA 60
CA 62

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GATCTGTGTA AGAAGTCTGA TATCGATGAA GATTCCGCTA CAGAAACCTG CAGCACATG 59

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AATTCATGTG CTGCAGGTTT CTGTAGCGGA ATCTTCATCG ATATCAGACT TCTTACACA 59

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GATCTGTCTA AGAAGTCTGA TATCGATGAA GATTACAGAT TCTTCAGACT ATAGCTACTT 60

CTAA 64

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AATCTTCATC GATATCAGAC TTCTTAGACA 30

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GATCTGGTTA AGAAGTCTGA TATCGATGAA GATTACCAAT TCTTCAGACT ATAGCTACTT 60

CTAA 64

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

AATCTTCATC GATATCAGAC TTCTTAACCA 30

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATTGTCCAGC TCTACCTCTG TTGGATCACA CTTCTTACAC A 41

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ACTCAAAGCA ACATTTGCGA TGAGGACAGC GCTACAGAAA CCTGCA 46

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GGTTTCTGTA GCGCTCTGCT CATCGCAAAT GTTGCTTTGA GTCGCAGTGA CTATCTG

57

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GCACCTACGA TAGGAACAAA TGCTACACGG CCGTGGTTCC GCTCGTGTAT GGTGGAGAG

59

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GAGCGGAACC ACGGCCGTGT AGCATTTGTT CCTATCGTAG GTGCTGCA

48

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACAAAAATGG TGGAAACTGC CCTTACGCCC GATGCATGCT ATCCGGACTG

50

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AATTCAGTCC GGATAGCATG CATCGGGCGT AAGGGCAGTT TCCACCATTT TTGTCTCTCC

60

ACCATACAC

69

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAAAAATGG TGGAAACTGC CCTTACGCCC GATGCATGCT ATCCGGACAA GGATGAATTG

60

TG

62

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AATTCACAAT TCATCCTTGT CCGGATAGCA TGCATCGGGC GTAAGGGCAG TTTCCACCAT 60
TTTGTCTCT CCACCATACA C 81

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GATCAGGTCG CTGCCATCCA AGACCCGAGG CTGTTCGCCG AAGAGAAGGC CGTCGCTGAC 60
TCCAAGTGCA AGTGTGCTCG TATTACTT 88

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CTAGAAGTAA TACGAGCACA CTTGCACTTG GAGTCAGCGA CGGCCTTCTC TTCGGCGAAC 60
AGCCTCGGGT CTTGGATGGC AGCGACCT 88

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TGGTACGAAT TCCAGGTSMA RCTGCAGSAG TCRG

34

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

ACAGATATCG GGATTTCTCG CAGACTC

27

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ACAGAATATC GTCAACACCT TCCCACCC

28

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ACAAAGCTTT TATTTACCCG ACAGACGGTC

30

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTCCCCCTC GAGCGAYATY SWGMTSACCC ARTCT

35

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ACACTGCAGC AGTTGGTGCA GCATCAGC

28

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CTGCAGGAAG CGGAAGCGGA GGAAGCGGAA GCGGAGGAAG CGGAAGCGAA TTC

53

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CCTTCGCCTT CGCCTCCTTC GCCTTCGCCT CCTTCGCCTT CGCTTAA

47

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ACAGGATCCA TGGAAACCCC AGCGCAGCTT CTCTTCCTCC TGCTACTCTG GCTCCCAAGA

60

TACCACCGGA CCCGGG

76

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TGGTACAGAT CTAGGTSMAR CTGCAGSAGT CRG

33

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ACAGGAATTC AATTTTCTTG TCCACCTT

28

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GTTCTAGAGA YATYSWGMS ACCCARTCT

29

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ACACCGCGGC AGTTGGTGCA GCATCAGC

28

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ACAGGATCCA TGGAAACCCC AGCGCAGCTT CTCTTCCTCC TGCTACTCTG GCTCCCAGAT 60
 ACCACCGGAA GATCT 75

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ACAACTAGTA TGGAAACCCC AGCGCAGCTT CTCTTCCTCC TGCTACTCTG GCTCCCAGAT 60
 ACCACCGGAT CTAGA 75

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Val	Ala	Val	Gln	Ser	Ala	Gly	Thr	Pro	Ala	Ser	Gly	Ser
1				5							10	

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Cys Ala Ala Pro Lys Lys Lys Arg Lys Val

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Cys Ala Ala Lys Arg Pro Pro Ala Ala Ile Lys Lys Ala Ala Ala Gly
1 5 10 15
Gln Ala Lys Lys Lys Lys
20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

His Asp Glu Leu
1

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

CGCATGACGA CGATAAGGCC CAAACGGAGA CCTGTACTGT TGCGCCTCGT GAACGGCAAA

ACTGCGGATT CCCGGAA

77

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GTTTTGCCGT TCACGAGGCG CAACAGTACA GGTCTCCGTT TGGGCCTTAT CGTCGTCATC 60
GCTTCA 66

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTAACACCCT CTCAGTGCGC TAATAAAGGC TGCTGTTTTG ATGACACGGT ACGGGGCGTT 60
CCGTGGTGCT TC 72

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GCCCCGTACC GTGTCATCAA AACAGCAGCC TTTATTAGCG CACTGAGAGG GTGTTACTTC 60

CGGGAATCCG CA

72

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TACCCCAATA CAATTGACGT TCCGCCTGAA GAAGAGTGCG AGCCGTAAG

49

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

AATTCTTACG GCTCGCACTC TTCTTCAGGC GGCAAGTCAA TTGTATTGGG GTAGAAGCAC

60

CACGGAAC

68

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Pro Leu Gly Ile Ile Gly Gly
1 5

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Ile Ile Gly Gly
1

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Val	Arg	Asp	Gln	Ala	Gln	Glu	Asn	Arg	Ala	Ser	Gly	Asp	Ala	Gly	Ser
1				5					10					15	

Ala Asp Gly Gln Ser Arg Ser Ser Ser Ser Lys Val Leu Phe
20 25 30

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Val	Pro	Ser	Thr	Pro	Pro	Thr	Pro	Ser	Pro	Ser	Thr	Pro	Pro	Thr	Pro
1				5					10					15	

Ser Pro Ser Cys Cys His Pro Arg Leu
 20 25

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Glu Gln Lys Leu Ile Ser Glu Asp Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp
 1 5 10 15
 Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu
 20 25 30
 Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg
 35 40 45
 Pro Val Tyr His Leu Ser Asp Leu Cys Lys Lys Asp Glu Asp Ser Ala
 50 55 60
 Thr Glu Thr Cys
 65

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Cys Lys Cys Ala Arg Asp Ser Asp Ala Glu Thr Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Cys Met Cys Thr Arg Val Thr Ser Arg Ile Ile Pro Ser Thr Glu Asp
1 5 10 15

Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Val Val Pro Leu
20 25 30

Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Arg Asn
35 40 45

Pro Val Tyr His Leu Ser Asp Val Cys Lys Lys Asn Glu Asp Asp Gly
50 55 60

Val Pro Glu Thr Cys
65

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Cys Gln Cys Val Arg Ile Thr Ser Arg Ile Ile Arg Asp Pro Asp Asn
 1 5 10 15
 Pro Ser Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu
 20 25 30
 Asn Thr Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Glu
 35 40 45
 Pro Lys Tyr Asn Leu Ala Asn Leu Cys Lys Lys Pro Asp Asp Asp Tyr
 50 55 60
 Ser Glu Thr Cys
 65

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Cys Lys Cys Val Lys Ile Ser Ser Arg Phe Val Pro Ser Thr Glu Arg
 1 5 10 15
 Pro Gly Glu Glu Ile Leu Glu Arg Asn Ile Gln Ile Thr Ile Pro Thr
 20 25 30
 Ser Ser Arg Met Xaa Ile Ser Asp Pro Tyr Ser Pro Leu Arg Thr Gln
 35 40 45
 Pro Val Tyr Asn Leu Trp Asp Ile Cys Gln Lys Xaa Ser Xaa Pro Asp
 50 55 60
 Asp Glu Cys
 65

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

```

Cys Met Cys Thr Arg Val Thr Ala Arg Ile Arg Gly Thr Arg Glu Asp
1          5          10          15
Pro Asn Glu Asp Ile Val Glu Arg Tyr Ile Arg Ile Asn Val Pro Leu
          20          25          30
Lys Asn Arg Gly Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Asn Gln
          35          40          45
Pro Val Tyr His Leu Ser Pro Ser Cys Lys Lys Tyr Pro Asp Gln Gly
          50          55          60
Val Pro Gln Ser Cys
65

```

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

```

Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Pro Ser Ala Glu Asp
1          5          10          15
Pro Ser Gln Asp Ile Val Glu Arg Asn Val Arg Ile Ile Val Pro Leu
          20          25          30
Asn Ser Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Met Arg Thr Lys
          35          40          45
Pro Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Thr Thr Glu
          50          55          60
Val Glu Leu Glu Asp Gln Val Val Thr Ala Ser Gln Ser Asn Ile Cys
65          70          75          80
Asp Ser Asp Ala Glu Thr Cys
          85

```

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121;

Cys Met Cys Thr Arg Val Thr Ser Arg Ile Ile Pro Ser Thr Glu Asp
1 5 10 15

Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Val Val Pro Leu
20 25 30

Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Arg Asn
35 40 45

Pro Val Tyr His Leu Ser Asp Val Cys Lys Lys Cys Asp Pro Val Glu
50 55 60

Val Glu Leu Glu Asp Gln Val Val Thr Ala Thr Gln Ser Asn Ile Cys
65 70 75 80

Asn Glu Asp Asp Gly Val Pro Glu Thr Cys
85 90

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Cys Gln Cys Val Arg Ile Thr Ser Arg Ile Ile Arg Asp Pro Asp Asn
1 5 10 15

Pro Ser Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu
20 25 30

Asn Thr Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Glu

35 40 45
 Pro Lys Tyr Asn Leu Ala Asn Leu Cys Lys Lys Cys Asp Pro Thr Glu
 50 55 60
 Ile Glu Leu Asp Asn Gln Val Phe Thr Ala Ser Gln Ser Asn Ile Cys
 65 70 75 80
 Pro Asp Asp Asp Tyr Ser Glu Thr Cys
 85

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Cys Lys Cys Val Lys Ile Ser Ser Arg Phe Val Pro Ser Thr Glu Arg
 1 5 10 15
 Pro Gly Glu Glu Ile Leu Glu Arg Asn Ile Gln Ile Thr Ile Pro Thr
 20 25 30
 Ser Ser Arg Met Xaa Ile Ser Asp Pro Tyr Ser Pro Leu Arg Thr Gln
 35 40 45
 Pro Val Tyr Asn Leu Trp Asp Ile Cys Gln Lys Cys Asp Pro Val Gln
 50 55 60
 Leu Glu Ile Gly Gly Ile Pro Val Leu Ala Ser Gln Pro Xaa Xaa Ser
 65 70 75 80
 Xaa Pro Asp Asp Glu
 85

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 86 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Cys Met Cys Thr Arg Val Thr Ala Arg Ile Arg Gly Thr Arg Glu Asp
 1 5 10 15
 Pro Asn Glu Asp Ile Val Glu Arg Tyr Ile Arg Ile Asn Val Pro Leu
 20 25 30
 Lys Asn Arg Gly Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Asn Gln
 35 40 45
 Pro Val Tyr His Leu Ser Pro Ser Cys Lys Lys Cys Asp Pro Tyr Glu
 50 55 60
 Asp Gly Val Val Thr Ala Thr Glu Thr Asn Ile Cys Tyr Pro Asp Gln
 65 70 75 80
 Gly Val Pro Gln Ser Cys
 85

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Gln Asp Glu Asn Glu Arg Ile Val Val Asp Asn Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Asp	Asp	Glu	Ala	Thr	Ile	Leu	Ala	Asp	Asn	Lys
1				5					10	

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Asp	Asp	Glu	Ala	Thr	Ile	Leu	Ala	Asp	Asn	Lys
1				5					10	

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Glu	Gln	Glu	Tyr	Ile	Leu	Ala	Asn	Asn	Lys
1				5					10

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Tyr Thr Tyr Asp Arg Asn Lys
1 5

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Tyr Thr Tyr Asp Arg Asn Lys
1 5

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Tyr Met Tyr Asp Arg Asn Lys
1 5

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Tyr Thr Tyr Asp Arg Asn Lys
1 5

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Arg Asp Tyr Cys Pro Glu Leu Asp Arg Asn Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met
1 5 10 15

Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp
20 25

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Cys Tyr Thr Asn Arg Val Lys Leu Ser Tyr Arg Gly Gln Thr Lys Met
1 5 10 15

Val Glu Thr Ala Leu Thr Pro Asp Ser Cys Tyr Pro Asp
20 25

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Cys Tyr Thr Thr Met Val Pro Leu Arg Tyr His Gly Glu Thr Lys Met
1 5 10 15

Val Gln Ala Ala Leu Thr Pro Asp Ser Cys Tyr Pro Asp
20 25

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Cys Tyr Thr Thr Leu Val Pro Ile Thr His Arg Gly Val Thr Arg Met
1 5 10 15

Val Lys Ala Thr Leu Thr Pro Asp Ser Cys Tyr Pro Asp
20 25

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Cys Tyr Thr Thr Glu Val Asn Phe Lys Lys Lys Val Pro Leu Thr Pro
 1 5 10 15

Asp Ser Cys Tyr Glu Tyr Ser Glu
 20

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Cys Tyr Thr Val Leu Val Pro Pro Gly Tyr Thr Gly Glu Thr Lys Met
 1 5 10 15

Val Gln Asn Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp
 20 25